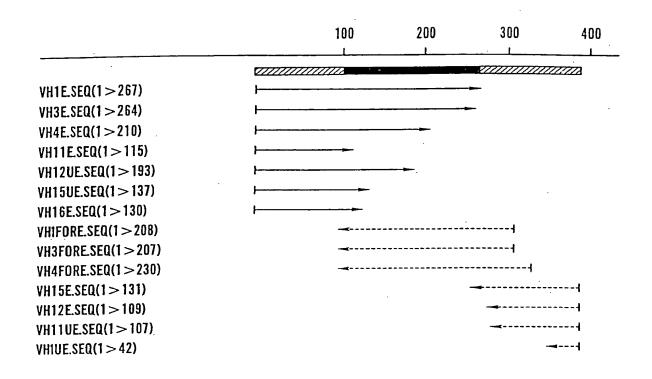


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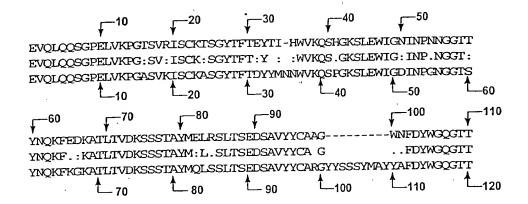
ENZYMES: ALL 74 ENZYMES (NO FILTER)
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

Dde I Alu I	Ava II Eco57 I
Pet   Avail Pyull	Sauce 1   .
	Bsrl
SEQ. ID. NO. 1 TCTCCTGTCAGGAACTGCAGGTGTCCTCTGGAGGTCCAGCTGCAACA	GICIGACCIGAACTGGIGAAG
SEQ. ID.NO.2 AGAGGACAGICCITCACGICCACAGGAGACACTCCAGGICGACGITGI	
SEQ.ID.NO.3 S P V R N C R C P L . G P A A T	V W T . T G E
SEQ.ID.NO.4 L L S G T A G V L S E V Q L Q Q	SGPELVK
SEQ.ID.NO.5 L S C Q E L Q V S S L R S S C N S	S L D L N W . S
Hph I	Dra III
Bsp6 II   EcoR V	Bsrt
SEO. ID. NO.1 CCTGGGACTTCAGTGAGGATATCCTGCAAGACTTCTGGATACACATTCA	ACTICATE TATACTACTACACTAC
<del></del>	+++++++++++++++++++++++++++++++++++++++
SEQ.ID.NO.2 GGACCCIGAAGICACTCCIATAGGACGITCIGAAGACCTATGIGIAAGI SEQ.ID.NO.3 A W D F S E D I L Q D F W I H I H	
	I.IYHTLG TEYTIHW
SEQ.ID.NO.5 L G L Q . G Y P A R L L D T H S	
Hph )	Rsal
Nco I	Kpn I
SEO.ID.NO.1 TGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAAACATCAATCC	 TAACAATTETTEACAAAT
<del>                                      </del>	<del>                                      </del>
SEQ.ID.NO.2 ACTICGICIOGIACCITICIOGAACTCACCIAACCITIGIAGITAGG SEO.ID.NO.3 E A E P W K E P . V D W K H O S	
SEQ.ID.NO.3 E A E P W K E P V D W K H Q S SEO.ID.NO.4 V K Q S H G K S L E W I G N I N P	
SEO.ID.NO.5 · S R A M E R A L S G L E T S I	
Lister de la	Alu I
IB	srl Ban II
Taq I Hae III Acc I	Rsa    Sac
SEQ. ID. NO. 1 CAATCAGAAGITGGAGGACAAGGCCACATTGACTGTAGACAAGTCCTCC	AGTACAGCCTACATGGAGCTC
SEO. ID. NO. 2 GITAGICTICAAGCICCIGITCCCGIGIAACICACATCIGITCAGGACG	
	Q Y S L H G A
SEQ.ID.NO.4 N Q K F E D K A T L T V D K S S	STAYMEL
SEQ.ID.NO.5 T I R S S R T R P H . L . T S P P	VQPTWSS
	<del></del>
	Sau96 I
Alu I  Dde     Hinf       Pst         Pvu   I	Bsr I       Hae III
SEQ. ID.NO.1 CGCAGCCTAACATCTGAGGATTCTGCAGTCTATTATTGTGCAGCTGGTTC	
<del></del>	<del></del>
SEQ. ID.NO.2 GOGTOGGATTGTAGACTCCTAAGACGTCAGATAATAACACGTCGACCAAC	
SEQ.ID.NO.3 P Q P N I . G F C S L L L C S W L	
SEQ.ID.NO.4 R S L T S E D S A V Y Y C A A G W	
SEQ.ID.NO.5 A A . H L R I L Q S I I V Q L V	
Alw26 I . Dde I	
SEQ. ID. NO. 1 AAGGCACCACTCTCACAGTCTCCTCAGCCAAAACGACACCC	
SEQ.ID.NO.3 R H H S H S L L S Q N D T	
SEQ.ID.NO.4 Q G T T L T V S S A K T T P	
SEQ.ID.NO.5 K A P L S Q S P Q P K R H P	FIG. 7

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### LIPMAN-PEARSON PROTEIN ALIGNMENT KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) SEQ2(1>125)	SEQ2(1>125)	SIMILARITY	GAP	GAP	CONSENSUS
J591VH.PRO MUVHIIA.PRO	MUVHIIA.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>115)	(1>125)	75.6	2	10	125



LTVSS :TVSS VTVSS

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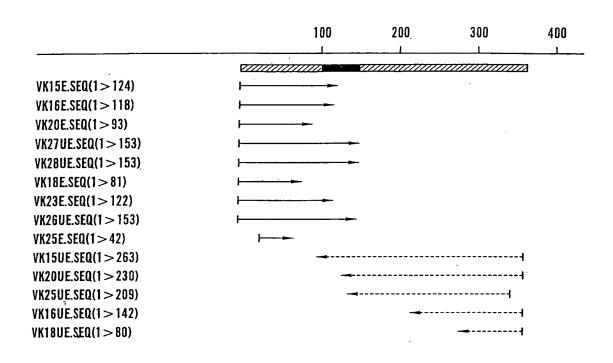


FIG. 9

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**ENZYMES:** 

SETTINGS:

ALL 74 ENZYMES (NO FILTER): LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

, Alu
Alu
SEQ. ID. NO. 9 TTATATGCACCTGATGCGAACATTGTAATGACCCAAATCTCCCCAAATCCATGTCCATGTCAGTAGCACACATTGTAATGACCCCAAATCTCCCCAAATCCATGTCCATGTCAGTAGCACACATTGTAATGACCCCAAATCTCCCCAAATCCCATGTCCATGTCAGTAGCACACATTGTAATGACCCCAAATCTCCCCAAATCCCATGTCCATGTCAGTAGCACACACA
SEQ. ID.NO.10 AATATACCTOGACTACCCTTGTAACATTACTGGGTTAGAGGGTTTAGGTACAGGTACAGTCATCCTCTCT
SEO.ID.NO.11 LYGADGNIVMTQSPKSMSMSVGE
PROTENTIAL Y M E L M G T L P N L P N P C P C Q . E R
SEQ.ID.NO.13 I I W S . W E H C N D P I S Q I H V H V S R R E
Hae III
GEQ. ID. NO. 9 GGCCACCTGACCTGCAAGCCAGGCAGGCAGGCAGGCAGGC
SEQ.ID.NO.11 R V T L T C K A S E N V V T Y V S W Y Q Q K P E
SEQ.ID.NO.12 G S P . P A R P V R M W L L M F P G I N R N Q
EQ.ID.NO.13 G H L D L Q G Q . E C G Y L C F L V S T E T R
Ava II Mbo I
Hpa II Bsr I   Dpn I
Alw26 I   Fok I   Rsa I   Sau 96 I   Bsa 0 I   Pvu I
TO COMPANY TO THE PROPERTY OF
EQ.ID.NO.19 GCAGICICCIAAACIGCIGAIAIAGGGGCAICCAACGGIAGAACIGICCGCAIGIGCGAAACIGICCGAIAIAGGGCAIGIGCGCAIGIGCGAAACIGICCGAAACIGICCGGAAACIGICCGGAAACIGICCGGAAACIGICCGAAACIGGAAACIGICCGAAACIAAAAAAAA
SEQ.ID.NO.11 QSPKLLIYGASNRIIGVPDRIIG SEQ.ID.NO.12SSLLNC.YTGHPTGTLGSPIASQA
EQ.ID.NO.12
SQ.ID.NO.13 A V S LILLA V. LA
I Mho I
Mbo I Eco57 I Bsp6 II Mbo II
Dpn I Bsp6 II Mbo II
Dpn I Bsp6 II Mbo II    SEQ. ID. NO. 9 AGIGGATCIGCAACAGATTICACTCIGACCATCAGCAGIGIGCAGGCTGAAGACCTTGCAGATTATCACT  280
Dpn I Bsp6 II Mbo II    EEQ. ID. NO. 9 AGIGGATCIGCAACAGATTTCACTCIGACCATCAGCAGGIGIGCAGGCTGAAGACCTTGCAGATTATCACT
Dpn I  EQ. ID. NO. 9 AGIGGATCIGCAACAGATTICACICIGACCATCAGCAGIGIGCAGGCICAAGACCITIGCAGATTATCACT  FHI HIH HIH HIH HIH HIH HIH HIH HIH HIH
Dpn I  EQ. ID. NO. 9  AGIGCATCIGCAACAGATTICACICICACCATCAGCAGIGIGCAGGCTCAAGACCTIGCAGATTATCACT  HHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
Dpn I  EQ. ID. NO.9  AGIGGATCIGCAACAGATTICACICIGACCATCAGCAGIGIGCAGGCTGAAGACCTIGCAGATTATCACT
Dpn I  SEQ. ID. NO. 9  AGIGGATCIGCAACAGATTICACICICACCATCAGCAGIGIGCAGGCIGAAGACCITGCAGATTATCACT  SEQ. ID. NO. 10  TCACCTAGACGITGICIAAAGICACACIGGIAGTCGACACGICGGACGICTAATAGICA  SEQ. ID. NO. 11  S G S A T D F T L T I S S V Q A E D L A D Y H  SEQ. ID. NO. 12  V D L Q Q I S L . P S A V C R L K T L Q I I T  SEQ. ID. NO. 13  Q W I C N R F H S D H Q Q C A G . R P C R L S L  AVA II  AVA II
Dpn I  Dp
Dpn I  SEQ. ID. NO. 9  AGIGGATCIGCAACAGATTICACICIGACCATCAGCAGIGIGCAGGCTGAAGACCTIGCAGATTATCACT  SEQ. ID. NO. 10  TCACCTAGACGITGICTAAAGIGACACTGGTAGTCGICACAGGTCCGACTTCTGCAACGICTAATAGIGA  SEQ. ID. NO. 11  S G S A T D F T L T I S S V Q A E D L A D Y H  SEQ. ID. NO. 12  V D L Q Q I S L P S A V C R L K T L Q I I T  SEQ. ID. NO. 13 Q W I C N R F H S D H Q Q C A G . R P C R L S L  AVA II  AVA II  SEQ. ID. NO. 9  GICCACAGGGTTACAGCTTACCGTACAGGTTCCCAGGGGGCACCAAGCTCGAAATAAAACGGCCTCATGC  SEQ. ID. NO. 9  GICCACAGGGTTACAGCTTACCGTACAGGTTCCCAGGGGGCACCAAGCTGCAAATAAAACGGCCTCATGC  SEQ. ID. NO. 9  GICCACAGGGTTACAGCTTACCGTACAGGTTCCCAGGGGGCACCAAGCTGCAAATAAAACGGCCTCATGC  SEQ. ID. NO. 9  GICCACAGGGTTACAGCTTACCGTACAGGTTCCCAGGGGGCACCAAGCTGCAAATAAAACGGCCTCCATGC
Dpn   Bsp6    Mbo        SEQ. ID. NO. 9   AGTGGATCTGCAACAGATTTCACTCTGACCATCACCAGGGGGCAGGCTGAAGACCTTGCAGAATTATCACT
Dpn   Bsp6    Mbo        SEQ. ID. NO. 9   AGIGGATCIGCAACAGATTICACTCICACCATCACCATCACCAGGIGIGCAGGCTCAACACCTIGCAGAATTATCACT
Dpn   Bsp6    Mbo
Dpn   Bsp6    Mbo        SEQ. ID. NO. 9   AGIGGATCIGCAACAGATTICACTCICACCATCACCATCACCAGGIGIGCAGGCTCAACACCTIGCAGAATTATCACT
Dpn   Bsp6    Mbo
Dpn   AGRICATICICAACACATITICACCATCAGCAGIGIGCAGGCTCAAGACCTTGCAGATTATCACT   HITTITITICAGACACACTTGCAGACACTTGCAGACTAGCAGTCTAATAGCACT   HITTITITICAGACACGTTGCAGACGTGTAAAGTCAACGTCTAATAGTCAACGTGTAAAGTCAAAGTCTAATAGTCAACGTGTAAAGTCAAAGTCTAATAGTCAACGTGTAAAGTCAAAGTCTAATAGTCAACGTGTAAAGTCAAAGTCTAATAGTCAACGTGTAAAGTCAAAGTCTAATAGTCAACGTGTAAAAGTCAAACGTCTAATAGTCAACGTGTAAACGTGTAAAAGTCAACGTGTAAACGTGTAAAAGTCAACGTGTAAACGTAACGTTAAAAACGACTTCAACGTATCAACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACGTTAACACCTTCAACACTTAATATTTTCCCCGAACTAACGTTAACGACTAACGACTAACACACTAACAACACTAACAACACTAACAACATAAAAAA
Dpn   Bsp6      Mbo
Dpn   Bsp6      Mbo
Dpn   Bsp6    Mbo

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### LIPMAN-PEARSON PROTEIN ALIGNMENT KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107)	SEQ2(1 > 1 1 1)	SIMILARITY	GAP	GAP	CONSENSUS
J591VK.PRO	MUVKV.PRO	INDEX	NUMBER	LENGTH	LENGTH
(1>107)	(1>109)	60.4	2	2	109

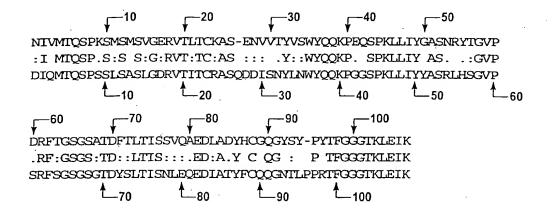


FIG. 11

